

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: DAVID GUZD Examiner #: 70677 Date: 7/27/04

Art Unit: 1636 Phone Number (415) 272-0767 Serial Number: 10/032585

Mail Box and Bldg/Room Location: PM: 2A79 Results Format Preferred (circle): PAPER DISK E-MAIL

Mailsy: 2C70

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please run a regular + interference sequence search
on SEQ ID NO: 4068 and 5068.

4068 NA 26
5068 1 20

Thanks

09 6u2585
7/28 3h

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:		NA Sequence (#)	STN _____
Searcher Phone #:		AA Sequence (#)	Dialog _____
Searcher Location:		Structure (#)	Questel/Orbit _____
Date Searcher Picked Up		Bibliographic	Dr.Link _____
Date Completed:		Litigation	Lexis/Nexis _____
Searcher Prep & Review Time		Fulltext	Sequence Systems _____
Clerical Prep. Time		Patent Family	WWW/Internet _____
On-line Time		Other	Other (specify) _____

Db	34539	ATTTTCAATTAGCTCAGGCTATGAAccc-----TTGGTATGAAcAAAGCTTACCG	34592	/db_xref="GI:30261"
Qy	596	GAGTGTCTTGCTTCTTACATCTTGTCAGTCAGTGGCAGCTGGTTGgaa	655	/db_xref="GO: P24391"
Db	34593	GTATTTACATATATCTTACTTCATCTTGTCAGTCAGTGGCAGCTGGTTGgaa	655	/translation="MAASSTPLAMDNAYSSSDAFNAQERKQFGLSNPCTI
Qy	656	CCATGCTCTCAAGAACCT-----TGCACCCAGCACAGCTTCTTATGTT	709	ETTAREVORDTILTYNMSGLADYFAFSLAPLFOVSHOFMGERLNIPYPAALYT
Db	34653	CTCTATGCAAAGGCTCTCTTCATGCCGCTGAAGAGAACCTTAAGTTGA	34712	NOIFAGQDNEGALISFRNFYDRITKTOFSIGEQDMAQFEHHLGDFASAK
Qy	710	CTCGTTATAGCAGGCAACTGGATGGCTACTGCACTTAAACGGTGGCAGGAG	766	AIMPSFLDQGILTFVGYLOQAVTPRIGLQAWQGQITQGDPDAYSFARYKGD
Db	34713	CTCGTTATAGCAGGCAACTGGATGGCTACTGCACTTAAACGGTGGCAGGAG	766	WVSAQLOQAGANTTSRKUDRVQAGWMTLSVRSQSMGGLTGIGITFGAKD
Qy	767	TGATGCAAGTTCGGAGAAGCTCATGATAAGTGAAGTGGTTAGAACCCAG	826	FRNTRQIDSKGLSLLERKIGAATUTRAADHIVTOQAKLNSVISASDVF
Db	34773	TCACGCCACATTGGGTAAGCTTGTGCTTCAAGGTTAGGGTAGATGTCGT	34832	LOSQEGAQSLNPP"
Qy	827	TGCGTCACTATGAAACAGTGCCTTCAATGATGGTGTGGTTGACAGCTA	886	
Db	34833	TATCACCTGGGATTAACCATCTTGCGCTTGTGATCAGTGCCTTCAACTG	34883	
Qy	887	TTGAGGTCAACTACTATGTCGCAAGTGGATAGATAAGAACTGCCCCTTGAGGTC	946	
Db	34884	CTGAGGTTACTCTGTCAGTGCCTTCAAGTGGTGCACAAAGTTATGIGTC	34943	
Qy	947	AATGGATCAAAAGGTAAGATCGTCATTTAGAAAGAAATCTGCAACTGTT	1006	
Db	34944	AAGTGAAGCAAGGTCGTCGTCACCCGTTA	35003	
Qy	1007	CCATATTTCGAAATGTC 1033		
Db	35004	CTCTGGCTTCTAGCTGATTAGTC 35030		
<hr/>				
RESULT 9				
NM0038	NCM0038	1453 bp	mRNA	linear
LOCUS	N.Crassa mRNA NM0038.			PLN 29-JUL-1992
DEFINITION	X56883			
ACCESSION	X56883			
VERSION	1			
KEYWORDS	GI:3025			
SOURCE	Neurospora crassa			
ORGANISM	Neurospora crassa			
REFERENCE	Kiebler, M.; Sordariomycetes; Sordariaceae; Neurospora.			
AUTHORS	Kiebler, M., Pfanner, R., Sollner, T., Griffiths, G., Horstmann, H., Pfanner, N. and Neupert, W.			
TITLE	Identification of a mitochondrial receptor complex required for recognition and membrane insertion of precursor proteins			
JOURNAL	Nature 348 (6302), 610-616 (1990)			
MEDLINE	9106645			
PUBMED	217414			
REFERENCE	(bases 1 to 1453)			
AUTHORS	Kiebler, M.			
JOURNAL	Submitted (26-JUN-1992) M. Kiebler, Institut f Physiologische Chemie, der LMU Muenchen, Goethestr. 8 Muenchen 2, FRG			
FEATURES	Location/Qualifiers			
source	1..1453			
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	/mol_type="mRNA"			
	/db_xref="Taxon:5141"			
gene	(clone lib="lambda gr11 cDNA"			
	1..1453			
	/gene="NM0038"			
	29..1078			
	/gene="NM0038"			
	/function=GIP (general insertion site)"			
	/codon_start=1 (outer membrane protein"			
	/protein_id="CAA40205.1"			
	975 ATTGAAAGAG 989			
<hr/>				
ORIGIN				
Query	Match	11.4%	Score	133.8;
Query	Best Local Similarity	51.8%	Pred. No.	4.4e-20;
Query	Matches	443;	Mismatches	382;
Query	Conservative	0;	Indels	30;
Query	Gaps	5;		
Db	138	CGATTTATATCACTATAAACGACACCGTAATCATGGTAAACACGGGAC	197	
Qy	97	CGATGCTTCAACGCTTCAGGAAAGGAAAGCTGGCTTTCGACCGGGAC	156	
Db	198	AATTAAACCTGACAAGAGGTTGCCGTTGATGTTTGGTCATATTCTTCAC	257	
Qy	157	GATCCGACCATCGCCGGAGGTCACCGGATACCCCTCTCACCAACTACATGTC	216	
Db	258	AGGTGAGGCTGTTAACAAAGCCTTGATCCACGATTCACATCCAACTCCA	317	
Qy	217	TGGCCCTCCGCGGAGTCACCAAGGTTCACTCTCCCTCTCCAGTTCCCA	276	
Db	318	CACTTAAGTGGATCCACGTTTACAGCTGTTAGGCTATGTCCTATGCCC	377	
Qy	277	CGAGTTGGCATGG--CGAGGTTGACCTTATGCTTCTGCTCTGAC	333	
Db	378	CGATGATTTCAGGTTAACATTGACATGATTATCATTTCTGAGATCA	437	
Qy	334	CGACGAGCTTCGGTCAGGTAACCTGGCAACAGAGGGCTCTCACAGATCA	393	
Db	438	TTCACGATGGCCAGTTGACATGACACCTTCAAGTCACATACATGGCTACACC	497	
Qy	394	CTACAGATGGGGTGAAGGACATACCAAGAGCGAGGCTCTGATTGGGGCCCA	450	
Db	498	ATCCATGATCAATTAGACAAGTAACTGATGATGTTGAGGTTGTTGATATT	617	
Qy	511	CATCACCC--CTCTTCTTGAGGGGCTCACCGTATCTGCTGGCTCCCTAAC	557	
Db	558	TTGACCCCTAACTTTATCAGGATGATGTTGAGGTTGTTGATGTTGAGTATT	617	
Qy	511	CTACAGATGGGGTGAAGGACATACCAAGAGCGAGGCTCTGATTGGGGCCCA	510	
Db	618	ACATCTTGTCATCAAGTGGAGTCGTTGGAAACCATGATCTCAAGAACATT	677	
Qy	568	CCAGCCGTCACCCAGCTCGCCCTGGCTCAGGCCGCTGGCACTGAGGCT	627	
Db	678	AGCACCA--CCAGCACAGCTGCTTCTATGCTGTTGTTGAGGACTCTAT	734	
Qy	628	CACTAGGGCCGACCGCTATCTTCTGAGGCTGACTGGGT	687	
Db	735	CGCTCTGTCACCCAGCTGCTTCTGAGGCTGTTGAGGAAAGTCAC	794	
Qy	688	TGCTAGCGTCAGCTCAGCTCAGGTCCTCTGAGGAGCTGAC	747	
Db	795	TGATGAGGAGCTGGTTGAGAACCAAGTGCCTGCACTATGAAACAGTTGCTG	854	
Qy	748	GGATGGGTCAGCTGGTTGA-----TATGAGCTATGTC	789	
Db	855	TCCATTAAGGTTGGGTTGAGGACTCATGAACTCAACTATGCGCA	914	
Qy	790	TCCCTCTAGAGCATGATGGTGCCTTACAGGAGCATCACACCTTGGCTCA	849	
Qy	915	GTATGATGAGACTGCGTTGAGGCTCATGGATTCAAGGAGTAGTCAGTC	974	
Db	850	GTACACTCGAGATGTCACCTCGACGCTGAGTCACCCAGGCACTGAGCTG	909	
Qy	975	ATTGAAAGAG 989		

Db	910 CTTGCTCGAGAGCG 924	Qy	856 CCATTAATGGTGTGGTTGACCACTCATGAAGCTAACACTATGGTCCAAAG 915
RESULT 10		Qy	424 -AATGATGGAGGCCATTAGA-----AGGAGGTCRCAACTSTGGCCAAAG 475
CNSID:DN1	CNS01DN1	Qy	916 TAGATAGAGAACTGCCTTTCAGAGGTCATGGATCAAGGTGATCTGCA 975
LOCUS	Botryotinia cinerea strain T4 cDNA library under conditions of nitrogen deprivation.	Db	476 TATATCTCAGATGTCATTCAGGCCAAGTGATCAACGGAAAGTGTGACTC 535
DEFINITION		Qy	976 TTITAGAGAGATCTGCACACTTTCATTTCTGGAGATTGATCA 1035
ACCESSION	AL117029	Db	536 TTATAGAGAAAGACTGCGCCACCTTGCACTTACTTGTGAGTGATGATCAT 595
VERSION	AL117029.1	Qy	
KEYWORDS	cDNA library; nitrogen deprivation.	Db	
SOURCE	Botryotinia fuckeliana	Qy	
ORGANISM	Botryotinia fuckeliana	Db	
BACTERIA; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.	REFERENCE	Qy	
REFERENCE	1. (bases 1 to 660)	Db	
AUTHORS	Bittin,F., Leviv,C., Fortini,D., Pradier,J.M. and Brysse,Y.	Qy	
TITLE	Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, Versailles, France	Db	
JOURNAL	2. (bases 1 to 660)	Qy	
REFERENCE	CP 5706 91057 EVRY cedex - FRANCE (E-mail : secrete@genoscope.cns.fr)	Db	
COMMENT	The cDNA library to be analyzed within the framework of this project was created using a Botryotinia cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the PBSII vector.	Qy	
FEATURES	Location/Qualifiers	Db	
SOURCE	1. 660 /organism="Botryotinia fuckeliana" /mol_type="mRNA" /strain="4" /db_xref="taxon:40559" /note="Genoscope sequence ID : W40B11"	Qy	
ORIGIN		Db	
Query Match 10.6%; Score 124.8; DB 8; Length 660; Best Local Similarity 56.0%; P-Value 5.7e-18; Matches 344; Conservative 0; Mismatches 252; Indels 18; Gaps 5;	COMMENT	Db	
Qy 439 TCGGATGGGACAATACTAACATCCAAAAGTCAATACATTAGCTCATGACACCA 498	REFERENCE	Qy	
11 TACAGATGGACTCAGCTTGTTCAGACGGAACTTCAGTGCCCCCTCA---A 67	AUTHORS	Db	
Qy 499 TCCATGATCCATTAGAACAGATAAAGCTATAGTATGTTCTATCATGCAACT 558	JOURNAL	Qy	
68 GCTATGATGCAATTAGAACAGATACTGGACAGAGATTCAGCTCAATCAACT 127	REFERENCE	Db	
559 TTAGCTCTACTTTATGGTAACTGATGAGTTGTTGGATCTGGATATTTA 618	COMMENT	Qy	
128 CTCAACCT--TCGATACTGGACGGAGATTTCGGGTTATGGTATATTA 184	ORGANISM	Db	
Db	This contig is an assembly of BAC 104 from 1 to: 70452, strain OR74, and cosmid 6B10 from 10453 to: 9076, cosmid library at the Fungal Generic Stock Center, BAC and cosmid clones are available Sequencing was performed by MWG Biotech AG, Ebersberg, Germany, http://www.mwg-mda.com	Qy	
Qy	Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groups II and V can be viewed at: http://mips.gsf.de/proj/neurospora.	Db	
Db	Location/Qualifiers	Qy	
Db	1. .90763 /organism="Neurospora crassa" /mol_type="Genomic DNA" /db_xref="taxon:5141" /chromosome="2"	Db	
Qy	misc_feature	Qy	
Db	1. .34518 /note="overlap to BAC contig 18F11, please refer to this entry for analysis and annotation" /gene="B10H4.01" /join(31067..31724..31779..31895..31970..322537..32610..32947, 33009..33198..33290..33516)	Qy	
Db	/gene="B10H4.010" /note="similarity to cholesterol oxidase (EC 1.1.3.6) precursor, Streptomyces sp., PIR:A12260" /codon_start=1 /product="related to cholesterol oxidase precursor" /protein_id="CAB21388.1" /db_xref="IGI-18376275" /db_xref="SPTRMBL-Q8X0NB" /translation="MDSLRAHQSNCAPSPPTPACSGHULGVKTDAGLFVGSHING	Qy	
Qy	365 GATAAGTGGAGCTGTTAGAACCAAGGTTGTGCACTTAACTGGAGGGTGTGAGCTGG- 423	Db	

OY	121	GTTTCACTGTCATCAGAACATGTTATACATGAACTGAAACCCGTAATCATTTGGGA	180
Db	193	GTTCATGATACATCACAGATGTTATACATGAAACCCGTAATCATTTGGGA	252
OY	181	TTRACCAAQCGGAGAACATGAAACTGAAACCCGTAATCATTTGGGA	240
Db	253	TTTACCAACCGGGAACATGAAACTGAAACCCGTAATCATTTGGGA	312
OY	241	GTCATATTCTACAGGGTGAGAGCTTACAGGGTGTGTTG	300
Db	313	GGTCATATTCTACAGGGTGAGAGCTTACAGGGTGTGTTG	372
OY	301	GCATTCACATCCACACTTGTAGATGATCAAGTTACACGCCATGCTTC	360
Db	373	GCATTCACATCCACACTTGTAGATGATCAAGTTACACGCCATGCTTC	432
OY	361	AGTCCTATGCAACCGTATGATATTCTTACAGGAACTGACATGATTTCA	420
Db	433	AGTCCTATGCAACCGTATGATATTCTTACAGGAACTGACATGATTTCA	492
OY	421	TTTCTGGTAGAGTCAATGAGCTTGTGAACTTACAGGAACTGACATGATTTCA	480
Db	493	TTTCTGGTAGAGTCAATGAGCTTGTGAACTTACAGGAACTGACATGATTTCA	552
OY	481	TTGCTCATGGACACCACATGATCCATTGAGACAGATTAACGTTAATGATGT	540
Db	553	TTGCTCATGGACACCACATGATCCATTGAGACAGATTAACGTTAATGATGT	612
OY	541	TCTTCATGCAACTTGTGACCTACTTTATCGGATGAACTGAGCTGAGTT	600
Db	613	TCTTCATGCAACTTGTGACCTACTTTATCGGATGAACTGAGCTGAGTT	672
OY	601	GTGTTGCACTTGTGACCTACTTTATCGGATGAACTGAGCTGAGTT	660
Db	673	GTGTTGCACTTGTGACCTACTTTATCGGATGAACTGAGCTGAGTT	732
OY	661	TACTCCAGCAACCTTGACCCACGACACAGCTGTCTATGTTGCTTATAAT	720
Db	733	TACTCCAGCAACCTTGACCCACGACACAGCTGTCTATGTTGCTTATAAT	792
OY	721	GAGGAACTGATGCTGCTGTCACCAAGCTGAGCTCGAGGTTCTATTGCAATT	780
Db	793	GCKGCHACTGGATGCCGCTGTCACCTCGACGCTGTTCTATTGCAATT	852
OY	781	TGGAGAAGGTCTGATTAAGTGCGAGCTGGTTAGAACCCAGTGCTGCCATTG	840
Db	853	TGGAGAAGGTCTGATTAAGTGCGAGCTGGTTAGAACCCAGTGCTGCCATTG	912
OY	841	AACCAAGTGTGATCCATTAACTGGTGTTGACCACTCATGAGGCTCAACT	900
Db	913	AACCAAGTGTGATCCATTAACTGGTGTTGACCACTCATGAGGCTCAACT	972
OY	901	ACTATGGTGCCAGTGTAGATGATGAACTGCGCTTTCAGAGTTCTATGATTAAG	960
Db	973	ACTATGGTGCCAGTGTAGATGATGAACTGCGCTTTCAGAGTTCTATGATTAAG	1032
OY	961	GTTAAGATCACTGCATTTGAAAGAAGATGATGCGGTTTCAGAGTTCTATGATTAAG	1020
Db	1033	GTTAAGATCACTGCATTTGAAAGAAGATGATGCGGTTTCAGAGTTCTATGATTAAG	1092
OY	1021	GGAGAAATGATCACTGAACTGATCTCGTTGGGTTGGTTCAATTGAGGT	1080
Db	1093	GGAGAAATGATCACTGAACTGATCTCGTTGGGTTGGTTCAATTGAGGT	1152
OY	1081	GCTGGTATGAGCAATTGAGTTAGTGAACAGGTTAGTCAGGCTATGTTATCT	1140
Db	1153	GCTGGTATGAGCAATTGAGTTAGTCAGGCTATGTTATCT	1212
OY	1141	ATCCGAGTGTCCAGCTCAGGTCTCTTG	1171
Db	1213	ATCCGAGTGTCCAGCTCAGGTCTCTTG	1243

RESULT 8
US-10-603-113-3520
; Sequence 3520, Application US/10603113
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US-10/603,113
; CURRENT FILING DATE: 2003-06-24
; PRIORITY APPLICATION NUMBER: US/09/248,796
; PRIORITY FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 28206
; SEQ ID NO 3520
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Candida albicans
; US-10-603-113-3520

Db 793 GCACGCACTGGATGCCTCTGCTCAACTCAAGGTGTTGAAAGTC 852
 Qy 781 TGGAGAAAGTCACTGATAAAGTCAGCTGGTTAGAACCGAGTGTGCACTG 840
 Db 853 TGGCAAAAGTCACTGATAAAGTCAGCTGGTTAGAACCGAGTGTGCACTG 912
 Qy 841 AACACAGTGCTGATCCATTATGGGTGGTTGACCGAGTGTGCACTG 900
 Db 913 AACACAGTGCTGATCCATTATGGGTGGTTGACCGAGTGTGCACTG 972
 Qy 901 ACTATGGTGCACATGATACTGAGCTGAGCTGAGCTGTTAGAACCGAGTGTGCACTG 960
 Db 973 ACTATGGTGCACATGATACTGAGCTGAGCTGAGCTGTTAGAACCGAGTGTGCACTG 1032
 Qy 961 GGTAGATCAGTCAGTCAGTGTAGAAAGAGATCAGCCAACTGTCAATTATTTCT 1020
 Db 1033 GGTAGATCAGTCAGTCAGTGTAGAAAGAGATCAGCCAACTGTCAATTATTTCT 1092
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 Db 1093 GGAGAATGATCAATCAAGATCATCTGTTGGGTTGGATTGAACTT 1152
 Qy 1081 GCTGTTATGACAATGATGTTAATGCAAACAGGTTACTCGAGCTATGGTATCT 1140
 Db 1153 GCTGTTATGACAATGATGTTAATGCAAACAGGTTACTCGAGCTATGGTATCT 1212
 Qy 1141 ATCCAGGTCCTCCAGCTCCAGGTTCT 1171
 Db 1213 ATCCAGTGTGTCCTCCAGGTTCT 1243
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 Db 673 GTTCTGGTGAATCAATAGGTTGGGACAATCAACATTCACAGTCACTTAC 552
 Qy 493 TTTCCTGGTAGATCAATAGGTTGGGACAATCAACATTCACAGTCACTTAC 592
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 Db 613 TCTACATGCAACATTTGAACTTATTCAGGTTAGTCAGGTTCAATGGATT 672
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 Db 853 TGGAGAGGTACTGATTAAGTCAGTGGGTTAGAACCCAGTGTGCACTG 912
 Qy 841 AACACAGTGCTGATCCATTATGGGTGGTTGACCGAGTGTGCACTG 900
 Db 913 AACACAGTGCTGATCCATTATGGGTGGTTGACCGAGTGTGCACTG 972
 Qy 901 ACTATGGTGCACATGATACTGAGCTGAGCTGAGCTGTTAGAACCGAGTGTGCACTG 960
 Db 973 ACTATGGTGCACATGATACTGAGCTGAGCTGAGCTGTTAGAACCGAGTGTGCACTG 1032
 Qy 1021 GGAGAATGATCAATCAAGATCATCTGTTGGGTTGGATTGAACTT 1080
 Db 1093 GGAGAATGATCAATCAAGATCATCTGTTGGGTTGGATTGAACTT 1152
 Qy 1081 GCTGTTATGACAATGATGTTAATGCAAACAGGTTACTCGAGCTATGGTATCT 1140
 Db 1153 GCTGTTATGACAATGATGTTAATGCAAACAGGTTACTCGAGCTATGGTATCT 1212
 Qy 1141 ATCCAGGTCCTCCAGCTCCAGGTTCT 1171
 Db 1213 ATCCAGTGTGTCCTCCAGGTTCT 1243
 RESULT 9 US-60-096-409-3520
 ; Sequence 3520, Application US/60096409A.
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-016P
 ; CURRENT APPLICATION NUMBER: US/60/096,409A
 ; CURRENT FILING DATE: 1998-06-13
 ; NUMBER OF SEQ ID NOS: 28206
 ; SEQ ID NO 3520
 ; LENGTH: 1260
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 ; US-60-096-409-3520
 Query Match 99.3%; Score 1164; DB 65; Length 1260;
 Best Local Similarity 99.7%; Pred No. 1; e-306; Matches 1167; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Matches 1167; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ATGTCACAGATATCCCTCATTCAGCTACAGTACAGAAGCTGCGTT 60
 Db 73 ATGTCACAGATATCCCTCATTCAGCTACAGTACAGAAGCTGCGTT 132
 Qy 61 AGTTGCTCAGTACACCAACCCAGCAAGGAAATGGATTGGTCAACCA 120
 Db 133 AGTTGCTCAGTACACCAACCCAGCAAGGAAATGGATTGGTCAACCA 192
 Qy 121 GTTTCAGTACATCAGGATTTATCACTTAAACGACACCGTAATCATGGGA 180
 Db 193 GTTTCAGTACATCAGGATTTATCACTTAAACGACACCGTAATCATGGGA 252
 Qy 181 TTAAACCAACCCGGAACTGAACTGAGCAAGAAGTGTGCGGTGATGGTT 240
 Db 253 TTAAACCAACCCGGAACTGAACTGAGCAAGAAGTGTGCGGTGATGGTT 312
 Qy 241 GGTCAATTCTCAGGGTGAGCTGATTACACACACCTTCATGATGCCA 300
 Db 313 GGTCAATTCTCAGGGTGAGCTGATTACACACACCTTCATGATGCCA 372
 RESULT 10 US-10-126-956-3118
 ; Sequence 3118, Application US/10326956
 ; GENERAL INFORMATION:
 ; APPLICANT: Bauer et al.
 ; TITLE OF INVENTION: Protein Complexes and Methods for their Use
 ; FILE REFERENCE: 220615
 ; CURRENT APPLICATION NUMBER: US/10/326, 956
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: EP 01 130 253.6
 ; PRIOR FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 3282